Claims:

1. A computer-readable medium comprising a plurality of digitally encoded values representing the levels of expression of a plurality of genes characteristic of R.A. including a plurality of genes selected from the group consisting of SOCS3 (CISH3); RAGE (AGER); LST-1 (LY117); serum amyloid (SAA) 1-3; HMG-1; S100 A8, A9, and A12; Secretory Leukocyte Protease Inhibitor (SLPI); glucocorticoid leucine zipper (GILZ); PTPN-18; GADD-45A and B; Legumain (PRSC1); follistatin-like 1 (FST1); lipocalin 2 (Lcn2); glucose phosphate isomerase (GPI); Serine Protease Inhibitor (SpiL); and TSG-6, in a cell characteristic of R.A.

2. The computer-readable medium of claim 1, comprising values representing levels of expression of at least 5 genes selected from the group consisting of SOCS3 (CISH3); RAGE (AGER); LST-1 (LY117); SAA 1-3; HMG-1; S100 A8, A9, and A12; SLPI; GILZ; PTPN-18; GADD-45A and B; Legumain (PRSC1); FST1; Lcn2; GPI; SpiL; and TSG-6.

3. A computer-readable medium comprising a plurality of digitally encoded values representing the levels of expression of at least 10 genes characteristic of R.A. in a cell characteristic of R.A.

4. The computer-readable medium of claim 3, comprising values representing levels of expression of at least 50% of the genes set forth in Tables 1-5.

5. The computer-readable medium of claim 1, further comprising at least one value representing a level of expression of at least one gene characteristic of R.A. in a normal counterpart cell.

6. The computer-readable medium of claim 1, wherein the values represent ratios of, or differences between, a level of expression of a gene characteristic of R.A. in a cell characteristic of R.A. and a level of expression of the gene in a normal counterpart cell.

7. The computer-readable medium of claim 1, wherein less than about 50% of the values on the computer-readable medium represent expression levels of genes which are not characteristic of R.A.

8. A computer system, comprising:

a database comprising values representing expression levels of a plurality of genes characteristic of R.A. including a plurality of genes selected from the group consisting of

SOCS3 (CISH3); RAGE (AGER); LST-1 (LY117); SAA 1-3; HMG-1; S100 A8, A9, and A12; SLPI; GILZ; PTPN-18; GADD-45A and B; Legumain (PRSC1); FST1; Lcn2; GPI; SpiL; and TSG-6, in a cell characteristic of R.A.; and,

a processor having instructions to,

receive at least one query value representing at least one level of expression of at least one gene represented in the database, and,

compare the at least one query value and the at least one database value.

9. A computer program for analyzing levels of expression of a plurality of genes characteristic of R.A. in a cell, the computer program being disposed on a computer readable medium and including instructions for causing a processor to:

receive query values representing levels of expression of a plurality of genes characteristic of R.A. in a cell, and,

compare the query values with levels of expression of the plurality of genes in a cell characteristic of R.A.

10. A composition comprising a plurality of detection agents of genes which are characteristic of R.A. including a plurality of genes selected from the group consisting of SOCS3 (CISH3); RAGE (AGER); LST-1 (LY117); SAA 1-3; HMG-1; S100 A8, A9, and A12; SLPI; GILZ; PTPN-18; GADD-45A and B; Legumain (PRSC1); FST1; Lcn2; GPI; SpiL; and TSG-6, which detection agents are capable of detecting the expression of the genes or the polypeptides encoded by the genes, and wherein less than about 50% of the detection agents are genes which are not characteristic of R.A.

11. The composition of claim 10, wherein the detection agents are isolated nucleic acids which hybridize specifically to nucleic acids corresponding to the genes.

12. The composition of claim 12, comprising isolated nucleic acids which hybridize specifically to at least five genes selected from the group consisting of SOCS3 (CISH3); RAGE (AGER); LST-1 (LY117); SAA 1-3; HMG-1; S100 A8, A9, and A12; SLPI; GILZ; PTPN-18; GADD-45A and B; Legumain (PRSC1); FST1; Lcn2; GPI; SpiL; and TSG-6.

13. The composition of claim 10, comprising isolated nucleic acids which hybridize specifically to at least 10 different genes characteristic of R.A.

14. The composition of claim 13, comprising isolated nucleic acids which hybridize specifically to at least 100 different genes characteristic of R.A.

15. A solid surface to which are linked a plurality of detection agents of genes which are characteristic of R.A. including a plurality of genes selected from the group consisting of SOCS3 (CISH3); RAGE (AGER); LST-1 (LY117); SAA 1-3; HMG-1; S100 A8, A9, and A12; SLPI; GILZ; PTPN-18; GADD-45A and B; Legumain (PRSC1); FST1; Lcn2; GPI; SpiL; and TSG-6, which detection agents are capable of detecting the expression of the genes or the polypeptides encoded by the genes, and wherein less than about 50% of the detection agents on the solid surface are not detecting genes characteristic of R.A.

16. The solid surface of claim 15, wherein the detection agents are isolated nucleic acids which hybridize specifically to the genes.

17. The solid surface of claim 16, wherein the detection agents are covalently linked to the solid surface.

18. A composition comprising antagonists of a plurality of genes characteristic of R.A. including a plurality of genes selected from the group consisting of SOCS3 (CISH3); RAGE (AGER); LST-1 (LY117); SAA 1-3; HMG-1; S100 A8, A9, and A12; SLPI; GILZ; PTPN-18; GADD-45A and B; Legumain (PRSC1); FST1; Lcn2; GPI; SpiL; and TSG-6.

19. The composition of claim 18, wherein the antagonists are antisense nucleic acids, siRNAs, ribozymes or dominant negative mutants.

20. A method for determining the difference between levels of expression of a plurality of genes characteristic of R.A. in a cell and reference levels of expression of the genes, comprising

providing RNA from a cell;

determining levels of RNA of a plurality of genes characteristic of R.A. including a plurality of genes selected from the group consisting of SOCS3 (CISH3); RAGE (AGER); LST-1 (LY117); SAA 1-3; HMG-1; S100 A8, A9, and A12; SLPI; GILZ; PTPN-18; GADD-45A and B; Legumain (PRSC1); FST1; Lcn2; GPI; SpiL; and TSG-6 to obtain the levels of expression of the plurality of genes in the cell; and

comparing the levels of expression of the plurality of genes in the cell to a set of reference levels of expression of the genes,

to thereby determine the difference between levels of expression of the plurality of genes characteristic of R.A. in the cell and reference levels of expression of the genes.

21. The method of claim 20, wherein the set of reference levels of expression includes the levels of expression of the genes in a subject having R.A.

22. The method of claim 21, wherein the set of reference levels of expression further includes the levels of expression of the genes in a subject who does not have R.A.

23. The method of claim 20, comprising incubating a nucleic acid sample derived from the RNA of the cell of the subject with nucleic acids corresponding to the genes, under conditions wherein two complementary nucleic acids hybridize to each other.

24. The method of claim 23, wherein the nucleic acids corresponding to the genes are attached to a solid surface.

25. The method of claim 20, comprising entering the levels of expression of the plurality of genes into a computer which comprises a memory with values representing the set of reference levels of expression.

26. The method of claim 25, wherein comparing the level comprises providing computer instructions to perform.

27. A method for determining whether a subject has or is likely to develop R.A., comprising obtaining a cell from the subject and comparing gene expression levels in the cell to those of a set of reference levels of expression, according to the method of claim 20, wherein similar levels of expression of the plurality of genes indicates that the subject has or is likely to develop R.A.

28. The method of claim 27, wherein the cell is a peripheral blood mononuclear cell (PBMC) and the set of reference levels of expression includes the levels of expression of the genes in a PBMC of a subject having R.A.

29. The method of claim 27, wherein the cell is a PBMC and the set of reference levels of expression includes the average of levels of expression of the genes in a PBMC of a plurality of subjects having R.A.

30. The method of claim 27, further comprising iteratively providing RNA from the subject and determining the level of RNA, such as to determine an evolution of the levels of expression of the genes in the subject.

31. A method for determining whether a therapy for R.A. is effective in a subject having R.A. who is receiving the therapy, comprising obtaining a cell from the subject and comparing levels of expression in the cell of the subject to those in subjects having R.A. and in subjects who do not have R.A., according to the method of claim 20, wherein levels of expression in the cell of the subject that are more similar to those of the subject having R.A. than the subject who does not have R.A. indicates that the therapy is not effective, whereas levels of expression in the cell of the subject that are more similar to those of the subject not having R.A. than the subject having R.A. indicates that the therapy is effective.

32. The method of claim 27, wherein the set of reference levels of expression is in the form of a database.

33. The method of claim 32, wherein the database is included in a computer-readable medium.

34. The method of claim 33, wherein the database is in communications with a microprocessor and microprocessor instructions for providing a user interface to receive expression level data of a subject and to compare the expression level data with the database.

35. The method of claim 27, comprising

obtaining a patient sample from a caregiver;

identifying expression levels of a plurality of genes characteristic of R.A. from the patient sample;

determining whether the levels of expression of the genes in the patient sample are more similar to those of a subject having R.A. or to those of a subject who does not have R.A.; and

transmitting the results to the caregiver.

36. The method of claim 35, wherein the results are transmitted across a network.

37. A method for identifying a compound for treating R.A., comprising

providing levels of expression of a plurality of genes characteristic of R.A. in a cell characteristic of R.A. incubated with a test compound;

providing levels of expression of a normal counterpart cell; and

comparing the two levels of expression, wherein similar levels of expression in the two cells indicates that the compound is likely to be effective for treating R.A.

38. A diagnostic or drug discovery kit, comprising a computer-readable medium of claim 1 and instructions for use.

39. A diagnostic or drug discovery kit, comprising a composition of claim 10 and instructions for use.

40. A diagnostic or drug discovery kit, comprising a solid surface of claim 15 and instructions for use.